

EXHIBIT "A"



Entrez

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

Bio

Search for

Go

Clear

Limits

Preview/Index

History

Clipboard

Details

Display

default

Show:

20

Send to

File

Get Subsequence

Fe

☐ 1: NP_620686. a disintegrin-lik...[gi:21265058]

BLink, Domains, Links

LOCUS NP_620686 950 aa linear PRI 05-OCT-2003

DEFINITION a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 15 preproprotein [Homo sapiens].

ACCESSION NP_620686

VERSION NP_620686.1 GI:21265058

DBSOURCE REFSEQ: accession [NM_139055.1](#)

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 950)

AUTHORS Cal,S., Obaya,A.J., Llamazares,M., Garabaya,C., Quesada,V. and Lopez-Otin,C.

TITLE Cloning, expression analysis, and structural characterization of seven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains

JOURNAL Gene 283 (1-2), 49-62 (2002)

MEDLINE [21856482](#)

PUBMED [11867212](#)

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from [AJ315733.1](#).

Summary: This gene encodes a member of the ADAMTS (a disintegrin and metalloproteinase with thrombospondin motifs) protein family. ADAMTS family members share several distinct protein modules, including a propeptide region, a metalloproteinase domain, a disintegrin-like domain, and a thrombospondin type 1 (TS) motif. Individual members of this family differ in the number of C-terminal TS motifs, and some have unique C-terminal domains. The protein encoded by this gene has a high sequence similarity to the proteins encoded by ADAMTS1 and ADAMTS8. The function of this protein has not been determined.

FEATURES

source

Location/Qualifiers

1..950

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="11"

/map="11q25"

Protein

1..950

/product="a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 15 preproprotein"

Region

67..180

/region_name="Reprolysin family propeptide. This region is the propeptide for members of peptidase family M12B. The propeptide contains a sequence motif similar to the

'cysteine switch' of the matrixins. This motif is found at the C terminus of the alignment but is not well aligned"

/note="Pep_M12B_propep"

/db_xref="CDD:pfam01562"

mat_peptide 206..950

/product="a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 15"

Region 218..427

/region_name="Reprolysin (M12B) family zinc metalloprotease. The members of this family are enzymes that cleave peptides. These proteases require zinc for catalysis. Members of this family are also known as adamalysins. Most members of this family are snake venom endopeptidases, but there are also some mammalian proteins and fertilin. Fertilin and closely related proteins appear to not have some active site residues and may not be active enzymes"

/note="Reprolysin"

/db_xref="CDD:pfam01421"

Region 437..506

/region_name="ADAM Cysteine-Rich Domain"

/note="ACR"

/db_xref="CDD:smart00608"

Region 519..571

/region_name="Thrombospondin type 1 repeats"

/note="TSP1"

/db_xref="CDD:smart00209"

Region 897..950

/region_name="Thrombospondin type 1 repeats"

/note="TSP1"

/db_xref="CDD:smart00209"

CDS 1..950

/gene="ADAMTS15"

/coded_by="NM_139055.1:1..2853"

/note="go_component: extracellular matrix [goid 0005578] [evidence IEA];

go_function: zinc ion binding [goid 0008270] [evidence IEA];

go_function: metalloendopeptidase activity [goid 0004222] [evidence IEA];

go_function: hydrolase activity [goid 0016787] [evidence IEA];

go_process: integrin-mediated signaling pathway [goid 0007229] [evidence IEA];

go_process: proteolysis and peptidolysis [goid 0006508] [evidence IEA]"

/db_xref="GeneID:170689"

/db_xref="LocusID:170689"

/db_xref="MIM:607509"

ORIGIN

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1 mlllgiltla fagrtaggse perevvvpir ldpdingrry ywrgpedsgd qglifqita
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121 gglrgafgyr gaeyvisplp nasapaaqrn sqgahllqrr gvpggpsgdp tsrsvgasgw
181 npailraldp ykprragfge srsrrrsgra krfvsipryv etlvvadesm vkfhgadleh
241 ylltllataa rlyrhpsiln pinivvvkvl llrdrdsgpk vtgnaaltlr nfcawqkkl
301 kvskdkhpeyw dtailftrqd lcgattcdtl gmadvgtmcd pkrsdcsvied dglpsaftta
361 helghvfnmp hdnvkvceev fgklranhmm sptliqidra npwsacsaa i tdfldsgghg
421 dclldqpskp islpedlpga sytllsqcel afgvgskpcp ymqyctklwc tgkakgqmv
481 qtrhfpwadg tscgeglcl kgacverhnl nkhrvdgsa kwdpygpcsr tcgggvqlar
541 rqctnptpan ggkycegvrv kyrsclnlep pssasgksfr eeqceafngy nhstnrltla

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601 vawvpkysgv sprdkcklic rangtgyfyv lapkvvdgtl cspdstsvcv qgkcikagcd
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721 gddnylalkn sqgkyllngh fvvsaverdl vvkgsllrys gtgtaveslq asrpileplt
781 vevlsvgkmt pprvrysfyl pkepredkss hpkdprgpsv lhnsvlslsn qveqpddrpp
841 arwvagswgp csascgsglq kravdcrgsa gqrtvpacda ahrpvetqac gepcptwels
901 awspcskscg rgfqrslkc vghggrllar dqcnlhrkpq eldfcvlrpc
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//

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Nov 3 2003 07:26:36

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

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vs /tmp/fastaNAAwSainL library
searching /tmp/fastaNAAwSainL library

950 residues in 1 sequences

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join: 39, opt: 27, gap-pen: -12/ -2, width: 16
Scan time: 0.017

The best scores are: opt
gi|21265058|ref|NP_620686.1| a disintegrin-like a (950) 6692

>>gi|21265058|ref|NP_620686.1| a disintegrin-like and me (950 aa)
initn: 6692 initl: 6692 opt: 6692
Smith-Waterman score: 6692; 100.000% identity in 950 aa overlap (1-950:1-950)

Lex	10	20	30	40	50	60
	MLLLGILTLAFAGRTAGGSEPEREVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF					
gi 212	MLLLGILTLAFAGRTAGGSEPEREVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF					
	10	20	30	40	50	60
Lex	70	80	90	100	110	120
	QEDFYHLHTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPDSFAAVSLC					
gi 212	QEDFYHLHTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPDSFAAVSLC					
	70	80	90	100	110	120
Lex	130	140	150	160	170	180
	GGLRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASGW					
gi 212	GGLRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASGW					
	130	140	150	160	170	180
Lex	190	200	210	220	230	240
	NPAILRALDPYKPRRAGFGESRSRRRSRAKRFVSI PRYVETLVVADESMVKFHGADLEH					
gi 212	NPAILRALDPYKPRRAGFGESRSRRRSRAKRFVSI PRYVETLVVADESMVKFHGADLEH					
	190	200	210	220	230	240
Lex	250	260	270	280	290	300
	YLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLN					
gi 212	YLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLN					
	250	260	270	280	290	300
Lex	310	320	330	340	350	360
	KVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTA					
gi 212	KVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTA					
	310	320	330	340	350	360
Lex	370	380	390	400	410	420
	HELGHVFNMPHDNVKVC EEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHG					

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gi|212 .....
HELGHVFNMPHDNVKVC EEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHG
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      430      440      450      460      470      480
Lex    DCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMV
      .....
gi|212 DCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMV
      430      440      450      460      470      480

      490      500      510      520      530      540
Lex    QTRHFPWADGTSCGEGKLCCLKGACVERHNLNKHVRVDGSAKWDPYGPCSRTC GGGVQLAR
      .....
gi|212 QTRHFPWADGTSCGEGKLCCLKGACVERHNLNKHVRVDGSAKWDPYGPCSRTC GGGVQLAR
      490      500      510      520      530      540

      550      560      570      580      590      600
Lex    RQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLA
      .....
gi|212 RQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLA
      550      560      570      580      590      600

      610      620      630      640      650      660
Lex    VAWVPKYSGVSPRDCKKLICRANGTG YFYVLAPKVVDGTL CSPDSTSVCVQ GKCIKAGCD
      .....
gi|212 VAWVPKYSGVSPRDCKKLICRANGTG YFYVLAPKVVDGTL CSPDSTSVCVQ GKCIKAGCD
      610      620      630      640      650      660

      670      680      690      700      710      720
Lex    GNLGSKKRFDKCGVCGGDNKSKKVTGLFTKPMHGYNFVVAIPAGASSIDIRQ RGYKGLI
      .....
gi|212 GNLGSKKRFDKCGVCGGDNKSKKVTGLFTKPMHGYNFVVAIPAGASSIDIRQ RGYKGLI
      670      680      690      700      710      720

      730      740      750      760      770      780
Lex    GDDNYLALKNSQGKYLLNGHFVVS AVERDLVVKGSLRLRYSGTGTAVESLQASRPILEPLT
      .....
gi|212 GDDNYLALKNSQGKYLLNGHFVVS AVERDLVVKGSLRLRYSGTGTAVESLQASRPILEPLT
      730      740      750      760      770      780

      790      800      810      820      830      840
Lex    VEVL SVGKMT PPRVRY SFYLPKEPREDKSSH PKDPRGPSVLHNSVLSLSNQVEQPDDRPP
      .....
gi|212 VEVL SVGKMT PPRVRY SFYLPKEPREDKSSH PKDPRGPSVLHNSVLSLSNQVEQPDDRPP
      790      800      810      820      830      840

      850      860      870      880      890      900
Lex    ARWVAGSWGPCSASCGSGLQKRAVD CRGSAGQRTVPACDA AHRPVETQACGEPCPTWELS
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      850      860      870      880      890      900

      910      920      930      940      950
Lex    AWSPCKSKCGRGFQRRSLKCVGHGGRLLARDQCNLHRKPQELDFCVLRPC
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gi|212 AWSPCKSKCGRGFQRRSLKCVGHGGRLLARDQCNLHRKPQELDFCVLRPC
      910      920      930      940      950
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950 residues in 1 query sequences
950 residues in 1 library sequences
Scomplib [version 3.3t05 March 30, 2000]
start: Thu Nov 20 13:16:59 2003 done: Thu Nov 20 13:16:59 2003
Scan time: 0.017 Display time: 1.250

Function used was FASTA